

DOCUMENT NUMBER: 102-123456

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 102

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: DP2.5(APC)

(ix) FEATURE:

(A) NAME/KEY: CDS

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(B) LOCATION: 34.8562

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGACTCGGAA ATGAGGTCCA AGGGTAGCCA AGG ATG GCT GCA GCT TCA TAT GAT	54
Met Ala Ala Ala Ser Tyr Asp	
1 5	
CAG TTG TTA AAG CAA GTT GAG GCA CTG AAG ATG GAG AAC TCA AAT CTT	102
Gln Leu Leu Lys Gln Val Glu Ala Leu Lys Met Glu Asn Ser Asn Leu	
10 15 20	
CGA CAA GAG CTA GAA GAT AAT TCC AAT CAT CTT ACA AAA CTG GAA ACT	150
Arg Gln Glu Leu Glu Asp Asn Ser Asn His Leu Thr Lys Leu Glu Thr	
25 30 35	
GAG GCA TCT AAT ATG AAG GAA GTA CTT AAA CAA CTA CAA GGA AGT ATT	198
Glu Ala Ser Asn Met Lys Glu Val Leu Lys Gln Leu Gln Gly Ser Ile	
40 45 50 55	
GAA GAT GAA GCT ATG GCT TCT TCT GGA CAG ATT GAT TTA TTA GAG CGT	246
Glu Asp Glu Ala Met Ala Ser Ser Gly Gln Ile Asp Leu Leu Glu Arg	
60 65 70	
CTT AAA GAG CTT AAC TTA GAT AGC AGT AAT TTC CCT GGA GTA AAA CTG	294
Leu Lys Glu Leu Asn Leu Asp Ser Ser Asn Phe Pro Gly Val Lys Leu	
75 80 85	
CGG TCA AAA ATG TCC CTC CGT TCT TAT GGA AGC CGG GAA GGA TCT GTA	342
Arg Ser Lys Met Ser Leu Arg Ser Tyr Gly Ser Arg Glu Gly Ser Val	
90 95 100	
TCA AGC CGT TCT GGA GAG TGC AGT CCT GTT CCT ATG GGT TCA TTT CCA	390
Ser Ser Arg Ser Gly Glu Cys Ser Pro Val Pro Met Gly Ser Phe Pro	
105 110 115	
AGA AGA GGG TTT GTA AAT GGA AGC AGA GAA AGT ACT GGA TAT TTA GAA	438
Arg Arg Gly Phe Val Asn Gly Ser Arg Glu Ser Thr Gly Tyr Leu Glu	
120 125 130 135	
GAA CTT GAG AAA GAG AGG TCA TTG CTT CTT GCT GAT CTT GAC AAA GAA	486
Glu Leu Glu Lys Glu Arg Ser Leu Leu Leu Ala Asp Leu Asp Lys Glu	
140 145 150	
GAA AAG GAA AAA GAC TGG TAT TAC GCT CAA CTT CAG AAT CTC ACT AAA	534
Glu Lys Glu Asp Trp Tyr Tyr Ala Gln Leu Gln Asn Leu Thr Lys	
155 160 165	
AGA ATA GAT AGT CTT CCT TTA ACT GAA ATT TTT TCC TTA CAA ACA GAT	582
Arg Ile Asp Ser Leu Pro Leu Thr Glu Asn Phe Ser Leu Gln Thr Asp	
170 175 180	
TTG ACC AGA AGG CAA TTG GAA TAT GAA GCA AGG CAA ATC AGA GTT GCG	630
Leu Thr Arg Arg Gln Leu Glu Tyr Glu Asp Gln Ile Arg Val Ala	
185 190 195	
ATG GAA GAA CAA CTA GGT ACC TGC CAG GAT ATG GAA AAA CGA GCA CAG	678
Met Glu Glu Gln Leu Gly Thr Cys Gln Asp Met Glu Lys Arg Ala Gln	
200 205 210 215	
CGA AGA ATA GCC AGA ATT CAG CAA ATC GAA AAG GAC ATA CTT CGT ATA	726
Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu Lys Asp Ile Leu Arg Ile	
220 225 230	
CGA CAG CTT TTA CAG TCC CAA GCA ACA GAA GCA GAG AGG TCA TCT CAG	774
Arg Gln Leu Gln Ser Gln Ala Thr Glu Ala Gln Arg Ser Ser Gln	
235 240 245	
AAC AAG CAT GAA ACC GGC TCA CAT GAT GCT GAG CGG CAG AAT GAA GGT	822
Asn Lys His Glu Thr Gly Ser His Asp Ala Glu Arg Gln Asn Glu Gly	
250 255 260	
CAA GGA GTG GGA GAA ATC AAC ATG GCA ACT TCT GGT AAT GGT CAG GGT	870
Gln Gly Val Gly Glu Ile Asn Met Ala Thr Ser Gln Asn Gly Gln Gly	
265 270 275	
TCA ACT ACA CGA ATG GAC CAT GAA ACA GCC AGT GTT TTG AGT TCT AGT	918
Ser Thr Thr Arg Met Asp His Glu Thr Ala Ser Val Leu Ser Ser Ser	
280 285 290 295	

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AGC ACA CAC TCT GCA CCT CGA AGG CTG ACA AGT CAT CTG GGA ACC AAG	966
Ser Thr His Ser Ala Pro Arg Arg Leu Thr Ser His Leu Gly Thr Lys	
300 305 310	
GAT GAT ATG TCG CGA ACT TTG CTA GCT ATG TCT AGC TCC CAA GAC AGC	1014
Asp Asp Met Ser Arg Thr Leu Leu Ala Met Ser Ser Gln Asp Ser	
330 335 340	
TGT ATA TCC ATG CGA CAG TCT GGA TGT CTT CCT CTC CTC ATC CAG CTT	1110
Cys Ile Ser Met Arg Gln Ser Gly Cys Leu Pro Leu Leu Ile Gln Leu	
345 350 355	
TTA CAT GGC AAT GAC AAA GAC TCT GTA TTG TTG GGA AAT TCC CGG GGC	1158
Leu His Gly Asn Asp Lys Asp Ser Val Leu Leu Gly Asn Ser Arg Gly	
360 365 370 375	
AGT AAA GAG GCT CGG GCC AGG GCC AGT GCA GCA CTC CAC AAC ATC ATT	1206
Ser Lys Glu Ala Arg Ala Arg Ala Ser Ala Ala Leu His Asn Ile Ile	
380 385 390 395	
CAC TCA CAG CCT GAT GAC AAG AGA GGC AGG CGT GAA ATC CGA GTC CTT	1254
His Ser Gln Pro Asp Asp Lys Arg Gly Arg Arg Glu Ile Arg Val Leu	
395 400 405	
CAT CTT TTG GAA CAG ATA CGC GCT TAC TGT GAA ACC TGT TGG GAG TGG	1302
His Leu Leu Glu Gln Ile Arg Ala Tyr Cys Glu Thr Cys Trp Glu Trp	
410 415 420	
CAG GAA GCT CAT GAA CCA GGC ATG GAC CAG GAC AAA AAT CCA ATG CCA	1350
Gln Glu Ala His Glu Pro Gly Met Asp Gln Asp Lys Asn Pro Met Pro	
425 430 435	
GCT CCT GTT GAA CAT CAG ATC TGT CCT GCT GTG TGT GTT CTA ATG AAA	1398
Ala Pro Val Glu His Gln Ile Cys Pro Ala Val Cys Val Leu Met Lys	
440 445 450 455	
CTT TCA TTT GAT GAA GAG CAT AGA CAT GCA ATG AAT GAA CTA GGG GGA	1446
Leu Ser Phe Asp Glu Glu His Arg His Ala Met Asn Glu Leu Gly Gly	
460 465 470 475	
CTA CAG GCC ATT GCA GAA TTA TTG CAA GTG GAC TGT GAA ATG TAT GGG	1494
Leu Gln Ala Ile Ala Glu Leu Leu Gln Val Asp Cys Glu Met Tyr Gly	
475 480 485	
CTT ACT AAT GAC CAC TAC AGT ATT ACA CTA AGA CGA TAT GCT GGA ATG	1542
Leu Thr Asn Asp His Tyr Ser Ile Thr Leu Arg Arg Tyr Ala Gly Met	
490 495 500	
GCT TTG ACA AAC TTG ACT TTT GGA GAT GTA GCC AAC AAG GCT ACG CTA	1590
Ala Leu Thr Asn Leu Thr Phe Gly Asp Val Ala Asn Lys Ala Thr Leu	
505 510 515	
TGC TCT ATG AAA GGC TGC ATG AGA GCA CTT GTG GCC CAA CTA AAA TCT	1638
Cys Ser Met Lys Gly Cys Met Arg Ala Leu Val Ala Gln Leu Lys Ser	
520 525 530 535	
GAA AGT GAA GAC TTA CAG CAG GTT ATT GCA AGT GTT TTG AGG AAT TTG	1686
Glu Ser Gln Asp Leu Gln Gln Val Ile Ala Ser Val Leu Arg Asn Leu	
540 545 550	
TCT TGG CGA GCA GAT GTA AAT AGT AAA AAG ACG TTG CGA GAA GTT GGA	1734
Ser Trp Arg Ala Asp Val Asn Ser Lys Lys Thr Leu Arg Glu Val Gly	
555 560 565	
AGT GTG AAA GCA TTG ATG GAA TGT GCT TTA GAA GTT AAA AAG GAA TCA	1782
Ser Val Lys Ala Leu Met Glu Cys Ala Leu Glu Val Lys Lys Glu Ser	
570 575 580 585	
ACC CTC AAA AGC GTA TTG AGT GCC TTA TGG ATT TTG TCA GCA CAT TGC	1830
Thr Leu Lys Ser Val Leu Ser Ala Leu Trp Asn Leu Ser Ala His Cys	
585 590 595	
ACT GAG AAT AAA GCT GAT ATA TGT GCT GTA GAT GGT GCA CTT GCA TTT	1878
Thr Glu Asn Lys Ala Asp Ile Cys Ala Val Asn Glu Ala Leu Ala Phe	
600 605 610 615	

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TTG	GTT	GGC	ACT	CTT	ACT	TAC	CGG	AGC	CAG	ACA	AAC	ACT	TTA	GCC	ATT	1926
Leu	Val	Gly	Thr	Leu	Thr	Tyr	Arg	Ser	Gln	Thr	Asn	Thr	Leu	Ala	Ile	
620							625						630			
ATT	GAA	AGT	GGA	GGT	GGG	ATA	TTA	CGG	AAT	GTG	TCC	AGC	TTG	ATA	GCT	1974
Ile	Glu	Ser	Gly	Gly	Gly	Ile	Leu	Arg	Asn	Val	Ser	Ser	Leu	Ile	Ala	
635							640						645			
ACA	AAT	GAG	GAC	CAC	AGG	CAA	ATC	CTA	AGA	GAG	AAC	AAC	TGT	CTA	CAA	2022
Thr	Asn	Glu	Asp	His	Arg	Gln	Ile	Leu	Arg	Glu	Asn	Asn	Cys	Leu	Gln	
650							655						660			
ACT	TTA	TTA	CAA	CAC	TTA	AAA	TCT	CAT	AGT	TTG	ACA	ATA	GTC	AGT	AAT	2070
Thr	Leu	Leu	Gln	His	Leu	Lys	Ser	His	Ser	Leu	Thr	Ile	Val	Ser	Asn	
665							670						675			
GCA	TGT	GGA	ACT	TTG	TGG	AAT	CTC	TCA	GCA	AGA	AAT	CCT	AAA	GAC	CAG	2118
Ala	Cys	Gly	Thr	Leu	Trp	Asn	Leu	Ser	Ala	Arg	Asn	Pro	Lys	Asp	Gln	
680							685						690			695
GAA	GCA	TTA	TGG	GAC	ATG	GGG	GCA	GTT	AGC	ATG	CTC	AAG	AAC	CTC	ATT	2166
Glu	Ala	Leu	Trp	Asp	Met	Gly	Ala	Val	Ser	Met	Leu	Lys	Asn	Leu	Ile	
700							705						710			
CAT	TCA	AAG	CAC	AAA	ATG	ATT	GCT	ATG	GGA	AGT	GCT	GCA	GCT	TTA	AGG	2214
His	Ser	Lys	His	Lys	Met	Ile	Ala	Met	Gly	Ser	Ala	Ala	Ala	Leu	Arg	
715							720						725			
AAT	CTC	ATG	GCA	AAT	AGG	CCT	GCG	AAG	TAC	AAG	GAT	GCC	AAT	ATT	ATG	2262
Asn	Leu	Met	Ala	Asn	Arg	Pro	Ala	Lys	Tyr	Lys	Asp	Ala	Asn	Ile	Met	
730							735						740			
TCT	CCT	GGC	TCA	AGC	TTG	CCA	TCT	CTT	CAT	GTT	AGG	AAA	CAA	AAA	GCC	2310
Ser	Pro	Gly	Ser	Ser	Leu	Pro	Ser	Leu	His	Val	Arg	Lys	Gln	Lys	Ala	
745							750						755			
CTA	GAA	GCA	GAA	TTA	GAT	GCT	CAG	CAC	TTA	TCA	GAA	ACT	TTT	GAC	AAT	2358
Leu	Glu	Ala	Glu	Leu	Asp	Ala	Gln	His	Leu	Ser	Glu	Thr	Phe	Asp	Asn	
760							765						770			775
ATA	GAC	AAT	TTA	AGT	CCC	AAG	GCA	TCT	CAT	CGT	AGT	AAG	CAG	AGA	CAC	2406
Ile	Asp	Asn	Leu	Ser	Pro	Lys	Ala	Ser	His	Arg	Ser	Lys	Gln	Arg	His	
780							785						790			
AAG	CAA	AGT	CTC	TAT	GGT	GAT	TAT	GTT	TTT	GAC	ACC	AAT	CGA	CAT	GAT	2454
Lys	Gln	Ser	Leu	Tyr	Gly	Asp	Tyr	Val	Phe	Asp	Thr	Asn	Arg	His	Asp	
795							800						805			
GAT	AAT	AGG	TCA	GAC	AAT	TTT	AAT	ACT	GGC	AAC	ATG	ACT	GTC	CTT	TCA	2502
Asp	Asn	Arg	Ser	Asp	Asn	Phe	Asn	Thr	Gly	Asn	Met	Thr	Val	Leu	Ser	
810							815						820			
CCA	TAT	TTG	AAT	ACT	ACA	GTG	TTA	CCC	AGC	TCC	TCT	TCA	TCA	AGA	GGA	2550
Pro	Tyr	Leu	Asn	Thr	Thr	Val	Leu	Pro	Ser	Ser	Ser	Ser	Ser	Arg	Gly	
825							830						835			
AGC	TTA	GAT	AGT	TCT	CGT	TCT	GAA	AAA	GAT	AGA	AGT	TTG	GAG	AGA	GAA	2598
Ser	Leu	Asp	Ser	Ser	Arg	Ser	Glu	Lys	Asp	Arg	Ser	Leu	Glu	Arg	Glu	
840							845						850			855
CGC	GGA	ATT	GGT	CTA	GGC	AAC	TAC	CAT	CCA	GCA	ACA	GAA	AAT	CCA	GGA	2646
Arg	Gly	Ile	Gly	Leu	Gly	Asn	Tyr	His	Pro	Ala	Thr	Glu	Asn	Pro	Gly	
860							865						870			
ACT	TCT	TCA	AAG	CGA	GGT	TTG	CAG	ATC	TCC	ACC	ACT	GCA	GCC	CAG	ATT	2694
Thr	Ser	Ser	Lys	Arg	Gly	Leu	Gly	Ile	Ser	Thr	Thr	Ala	Ala	Gly	Ile	
875							880						885			
GCC	AAA	GTC	ATG	GAA	GAA	GTG	TCA	GCC	ATT	CAT	ACC	TCT	CAG	GAA	GAC	2742
Ala	Lys	Val	Met	Glu	Glu	Val	Ser	Ala	Ile	His	Thr	Ser	Gln	Glu	Asp	
890							895						900			
AGA	AGT	TCT	GGG	TCT	ACC	ACT	GAA	TTA	CAT	TGT	GTG	ACA	GAT	GAG	AGA	2790
Arg	Ser	Ser	Gly	Ser	Thr	Thr	Glu	Leu	His	Cys	Val	Thr	Asp	Glu	Arg	
905							910						915			
AAT	GCA	CTT	AGA	AGA	AGC	TCT	GCT	GCC	CAT	ACA	CAT	TCA	AAC	ACT	TAC	2838
Asn	Ala	Leu	Arg	Arg	Ser	Ser	Ala	Ala	His	Thr	His	Ser	Asn	Thr	Tyr	
920							925						930			935

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AAT	TTC	ACT	AAG	TCG	GAA	AAT	TCA	AAT	AGG	ACA	TGT	TCT	ATG	CCT	TAT	2886
Asn	Phe	Thr	Lys	Ser	Glu	Asn	Ser	Asn	Arg	Thr	Cys	Ser	Met	Pro	Tyr	
940								945					950			
GCC	AAA	TTA	GAA	TAC	AAG	AGA	TCT	TCA	AAT	GAT	AGT	TTA	AAT	AGT	GTC	2934
Ala	Lys	Leu	Glu	Tyr	Lys	Arg	Ser	Ser	Asn	Asp	Ser	Leu	Asn	Ser	Val	
955								960					965			
AGT	AGT	AAT	GAT	GGT	TAT	GGT	AAA	AGA	GGT	CAA	ATG	AAA	CCC	TCG	ATT	2982
Ser	Ser	Asn	Asp	Gly	Tyr	Gly	Lys	Arg	Gly	Gln	Met	Lys	Pro	Ser	Ile	
970							975					980				
GAA	TCC	TAT	TCT	GAA	GAT	GAT	GAA	AGT	AAG	TTT	TGC	AGT	TAT	GGT	CAA	3030
Glu	Ser	Tyr	Ser	Glu	Asp	Asp	Glu	Ser	Lys	Phe	Cys	Ser	Tyr	Gly	Gln	
985							990				995					
TAC	CCA	GCC	GAC	CTA	GCC	CAT	AAA	ATA	CAT	AGT	GCA	AAT	CAT	ATG	GAT	3078
Tyr	Pro	Ala	Asp	Leu	Ala	His	Lys	Ile	His	Ser	Ala	Asn	His	Met	Asp	
1000							1005				1010				1015	
GAT	AAT	GAT	GGA	GAA	CTA	GAT	ACA	CCA	ATA	AAT	TAT	AGT	CTT	AAA	TAT	3126
Asp	Asn	Asp	Gly	Glu	Leu	Asp	Thr	Pro	Ile	Asn	Tyr	Ser	Leu	Lys	Tyr	
1020							1025						1030			
TCA	GAT	GAG	CAG	TTG	AAC	TCT	GGA	AGG	CAA	AGT	CCT	TCA	CAG	AAT	GAA	3174
Ser	Asp	Glu	Gln	Leu	Asn	Ser	Gly	Arg	Gln	Ser	Pro	Ser	Gln	Asn	Glu	
1035							1040						1045			
AGA	TGG	GCA	AGA	CCC	AAA	CAC	ATA	ATA	GAA	GAT	GAA	ATA	AAA	CAA	AGT	3222
Arg	Trp	Ala	Arg	Pro	Lys	His	Ile	Ile	Glu	Asp	Glu	Ile	Lys	Gln	Ser	
1050							1055					1060				
GAG	CAA	AGA	CAA	TCA	AGG	AAT	CAA	AGT	ACA	ACT	TAT	CCT	GTT	TAT	ACT	3270
Glu	Gln	Arg	Gln	Ser	Arg	Asn	Gln	Ser	Thr	Thr	Tyr	Pro	Val	Tyr	Thr	
1065							1070				1075					
GAG	AGC	ACT	GAT	GAT	AAA	CAC	CTC	AAG	TTC	CAA	CCA	CAT	TTT	GGA	CAG	3318
Glu	Ser	Thr	Asp	Asp	Lys	His	Leu	Lys	Phe	Gln	Pro	His	Phe	Gly	Gln	
1080							1085				1090				1095	
CAG	GAA	TGT	GTT	TCT	CCA	TAC	AGG	TCA	CGG	GGA	GCC	AAT	GGT	TCA	GAA	3366
Gln	Glu	Cys	Val	Ser	Pro	Tyr	Arg	Ser	Arg	Gly	Ala	Asn	Gly	Ser	Glu	
1100							1105						1110			
ACA	AAT	CGA	GTG	GGT	TCT	AAT	CAT	GGA	ATT	AAT	CAA	AAT	GTA	AGC	CAG	3414
Thr	Asn	Arg	Val	Gly	Ser	Asn	His	Gly	Ile	Asn	Gln	Asn	Val	Ser	Gln	
1115							1120						1125			
TCT	TTG	TGT	CAA	GAA	GAT	GAC	TAT	GAA	GAT	GAT	AAG	CCT	ACC	AAT	TAT	3462
Ser	Leu	Cys	Gln	Glu	Asp	Tyr	Glu	Asp	Asp	Asp	Lys	Pro	Thr	Asn	Tyr	
1130							1135					1140				
AGT	GAA	CGT	TAC	TCT	GAA	GAA	CAG	CAT	GAA	GAA	GAA	GAG	AGA	CCA		3510
Ser	Glu	Arg	Tyr	Ser	Glu	Glu	Glu	Gln	His	Glu	Glu	Glu	Glu	Glu	Arg	
1145							1150					1155				
ACA	AAT	TAT	AGC	ATA	AAA	TAT	AAT	GAA	GAG	AAA	CCT	CAT	GTG	GAT	CAG	3558
Thr	Asn	Tyr	Ser	Ile	Lys	Tyr	Asn	Glu	Glu	Lys	Arg	His	Val	Asp	Gln	
1160							1165				1170				1175	
CCT	ATT	GAT	TAT	AGT	TTA	AAA	TAT	GCC	ACA	GAT	ATT	CCT	TCA	TCA	CAG	3606
Pro	Ile	Asp	Tyr	Ser	Leu	Lys	Tyr	Ala	Thr	Asp	Ile	Pro	Ser	Ser	Gln	
1180							1185						1190			
AAA	CAG	TCA	TTT	TCA	TTC	TCA	AAG	AGT	TCA	TCT	GGA	CAA	AGC	AGT	AAA	3654
Lys	Gln	Ser	Phe	Ser	Phe	Ser	Lys	Ser	Ser	Ser	Gly	Gln	Ser	Ser	Lys	
1195							1200						1205			
ACC	GAA	CAT	ATG	TCT	TCA	AGC	AGT	GAG	AAT	ACG	TCC	ACA	CCT	TCA	TCT	3702
Thr	Glu	His	Met	Ser	Ser	Ser	Ser	Glu	Asn	Thr	Ser	Thr	Pro	Ser	Ser	
1210							1215					1220				
AAT	GCC	AAG	AGG	CAG	AAT	CAG	CTC	CAT	CCA	AGT	TCT	GCA	CAG	AGT	AGA	3750
Asn	Ala	Lys	Arg	Gln	Asn	Gln	Leu	His	Pro	Ser	Ser	Ala	Gln	Ser	Arg	
1225							1230					1235				
AGT	GGT	CAG	CCT	CAA	AAG	GCT	GCC	ACT	TGC	AAA	GTT	TCT	TCT	ATT	AAC	3798
Ser	Gly	Gln	Pro	Gln	Lys	Ala	Ala	Thr	Cys	Lys	Val	Ser	Ser	Ile	Asn	
1240							1245					1250				

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CAA GAA ACA ATA CAG ACT TAT TGT GTC GAA GAT ACT CCA ATA TGT TTT	3846
Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu Asp Thr Pro Ile Cys Phe	
1260 1265 1270	
TCA AGA TGT AGT TCA TTA TCA TCT TTG TCA TCA GCT GAA GAT GAA ATA	3894
Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser Ser Ala Glu Asp Glu Ile	
1275 1280 1285	
GGA TGT AAT CAG ACG ACA CAG GAA GCA GAT TCT GCT AAT ACC CTG CAA	3942
Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp Ser Ala Asn Thr Leu Gln	
1290 1295 1300	
ATA GCA GAA ATA AAA GGA AAG ATT GGA ACT AGG TCA GCT GAA GAT CCT	3990
Ile Ala Glu Ile Lys Gly Lys Ile Gly Thr Arg Ser Ala Glu Asp Pro	
1305 1310 1315	
GTG AGC GAA GTT CCA GCA GTG TCA CAG CAC CCT AGA ACC AAA TCC AGC	4038
Val Ser Glu Val Pro Ala Val Ser Gln His Pro Arg Thr Lys Ser Ser	
1320 1325 1330 1335	
AGA CTG CAG GGT TCT AGT TTA TCT TCA GAA TCA GCC AGG CAC AAA GCT	4086
Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu Ser Ala Arg His Lys Ala	
1340 1345 1350	
GTT GAA TTT CCT TCA GGA GCG AAA TCT CCC TCC AAA AGT GGT GCT CAG	4134
Val Glu Phe Pro Ser Gly Ala Lys Ser Pro Ser Lys Ser Gly Ala Gln	
1355 1360 1365	
ACA CCC AAA AGT CCA CCT GAA CAC TAT GTT CAG GAG ACC CCA CTC ATG	4182
Thr Pro Lys Ser Pro Pro Glu His Tyr Val Gln Glu Thr Pro Leu Met	
1370 1375 1380	
TTT AGC AGA TGT ACT TCT GTC AGT TCA CTT GAT AGT TTT GAG AGT CGT	4230
Phe Ser Arg Cys Thr Ser Val Ser Ser Leu Asp Ser Phe Glu Ser Arg	
1385 1390 1395	
TCG ATT GCC AGC TCC GTT CAG AGT GAA CCA TGC AGT GGA ATG GTA AGT	4278
Ser Ile Ala Ser Ser Val Gln Ser Glu Pro Cys Ser Gly Met Val Ser	
1400 1405 1410 1415	
GGC ATT ATA AGC CCC AGT GAT CTT CCA GAT AGC CCT GGA CAA ACC ATG	4326
Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp Ser Pro Gly Gln Thr Met	
1420 1425 1430	
CCA CCA AGC AGA AGT AAA ACA CCT CCA CCA CCT CCT CAA ACA GCT CAA	4374
Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro Pro Gln Thr Ala Gln	
1435 1440 1445	
ACC AAG CGA GAA GTA CCT AAA AAT AAA GCA CCT ACT GCT GAA AAG AGA	4422
Thr Lys Arg Glu Val Pro Lys Asn Lys Ala Pro Thr Ala Glu Lys Arg	
1450 1455 1460	
GAG AGT GGA CCT AAG CAA GCT GCA GTC AAT GCT GCA GTT CAG AGG GTC	4470
Glu Ser Gly Pro Lys Gln Ala Ala Val Asn Ala Ala Val Gln Arg Val	
1465 1470 1475	
CAG GTT CTT CCA GAT GCT GAT ACT TTA TTA CAT TTT GCC ACA GAA AGT	4518
Gln Val Leu Pro Asp Ala Asp Thr Leu Leu His Phe Ala Thr Glu Ser	
1480 1485 1490 1495	
ACT CCA GAT GGA TTT TCT TGT TCA TCC AGC CTG AGT GCT CTG AGC CTC	4566
Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser Leu Ser Ala Leu Ser Leu	
1500 1505 1510	
GAT GAG CCA TTT ATA CAG AAA GAT GTG GAA TTA AGA ATA ATG CCT CCA	4614
Asp Glu Pro Phe Ile Gln Lys Asp Val Gln Leu Arg Ile Met Pro Pro	
1515 1520 1525	
GTT CAG GAA AAT GAC AAT GGG AAT GAA ACA GAA TCA GAG CAG CCT AAA	4662
Val Gln Glu Asn Asp Asn Gly Asn Glu Thr Glu Ser Glu Gln Pro Lys	
1530 1535 1540	
GAA TCA AAT GAA AAC CAA GAG AAA GAG GCA GAA AAA ACT ATT GAT TCT	4710
Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala Glu Lys Thr Ile Asp Ser	
1545 1550 1555	
GAA AAG GAC CTA TTA GAT GAT TCA GAT GAT GAT GAT ATT GAA ATA CTA	4758
Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp Asp Asp Ile Glu Ile Leu	
1560 1565 1570 1575	

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GAA	GAA	TGT	ATT	ATT	TCT	GCC	ATG	CCA	ACA	AAG	TCA	TCA	CGT	AAA	GGC	4806
Glu	Glu	Cys	Ile	Ile	Ser	Ala	Met	Pro	Thr	Lys	Ser	Ser	Arg	Lys	Gly	
1580								1585						1590		
AAA	AAG	CCA	GCC	CAG	ACT	GCT	TCA	AAA	TTA	CCT	CCA	CCT	GTG	GCA	AGG	4854
Lys	Lys	Pro	Ala	Gln	Thr	Ala	Ser	Lys	Leu	Pro	Pro	Pro	Val	Ala	Arg	
1595								1600						1605		
AAA	CCA	AGT	CAG	CTG	CCT	GTG	TAC	AAA	CTT	CTA	CCA	TCA	CAA	AAC	AGG	4902
Lys	Pro	Ser	Gln	Leu	Pro	Val	Tyr	Lys	Leu	Leu	Pro	Ser	Gln	Asn	Arg	
1610							1615						1620			
TTG	CAA	CCC	CAA	AAG	CAT	GTT	AGT	TTT	ACA	CCG	GGG	GAT	GAT	ATG	CCA	4950
Leu	Gln	Pro	Gln	Lys	His	Val	Ser	Phe	Thr	Pro	Gly	Asp	Asp	Met	Pro	
1625							1630						1635			
CGG	GTG	TAT	TGT	GTT	GAA	GGG	ACA	CCT	ATA	AAC	TTT	TCC	ACA	GCT	ACA	4998
Arg	Val	Tyr	Cys	Val	Glu	Gly	Thr	Pro	Ile	Asn	Phe	Ser	Thr	Ala	Thr	
1640							1645					1650			1655	
TCT	CTA	AGT	GAT	CTA	ACA	ATC	GAA	TCC	CCT	CCA	AAT	GAG	TTA	GCT	GCT	5046
Ser	Leu	Ser	Asp	Leu	Thr	Ile	Glu	Ser	Pro	Pro	Asn	Glu	Leu	Ala	Ala	
1660							1665						1670			
GGA	GAA	GGA	GTT	AGA	GGA	GGA	GCA	CAG	TCA	GGT	GAA	TTT	GAA	AAA	CGA	5094
Gly	Glu	Gly	Val	Arg	Gly	Gly	Ala	Gln	Ser	Gly	Glu	Phe	Glu	Lys	Arg	
1675							1680						1685			
GAT	ACC	ATT	CCT	ACA	GAA	GGC	AGA	AGT	ACA	GAT	GAG	GCT	CAA	GGA	GGA	5142
Asp	Thr	Ile	Pro	Thr	Glu	Gly	Arg	Ser	Thr	Asp	Glu	Ala	Gln	Gly	Gly	
1690							1695						1700			
AAA	ACC	TCA	TCT	GTA	ACC	ATA	CCT	GAA	TTG	GAT	GAC	AAT	AAA	GCA	GAG	5190
Lys	Thr	Ser	Ser	Val	Thr	Ile	Pro	Glu	Leu	Asp	Asp	Asn	Lys	Ala	Glu	
1705							1710						1715			
GAA	GGT	GAT	ATT	CTT	GCA	GAA	TGC	ATT	AAT	TCT	GCT	ATG	CCC	AAA	GGG	5238
Glu	Gly	Asp	Ile	Leu	Ala	Glu	Cys	Ile	Asn	Ser	Ala	Met	Pro	Lys	Gly	
1720							1725					1730			1735	
AAA	AGT	CAC	AAG	CCT	TTC	CGT	GTG	AAA	AAG	ATA	ATG	GAC	CAG	GTC	CAG	5286
Lys	Ser	His	Lys	Pro	Phe	Arg	Vai	Lys	Lys	Ile	Met	Asp	Gln	Val	Gln	
1740							1745						1750			
CAA	GCA	TCT	GCG	TCG	TCT	TCT	GCA	CCC	AAA	AAA	AAT	CAG	TTA	GAT	GGT	5334
Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro	Asn	Asn	Gln	Leu	Asp	Gly		
1755							1760						1765			
AAG	AAA	AAG	AAA	CCA	ACT	TCA	CCA	GTA	AAA	CTT	ATA	CCA	CAA	AAT	ACT	5382
Lys	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val	Lys	Pro	Ile	Pro	Gln	Asn	Thr	
1770							1775						1780			
GAA	TAT	AGG	ACA	CGT	GTA	AGA	AAA	AAT	GCA	GAC	TCA	AAA	AAT	AAT	TTA	5430
Glu	Tyr	Arg	Thr	Arg	Vai	Arg	Lys	Asn	Ala	Asp	Ser	Lys	Asn	Asn	Leu	
1785							1790						1795			
AAT	GCT	GAG	AGA	GTT	TTC	TCA	GAC	AAQ	AAA	GAT	TCA	AAG	AAA	CAG	AAT	5478
Asn	Ala	Glu	Arg	Val	Phe	Ser	Asp	Asn	Lys	Asp	Ser	Lys	Lys	Gln	Asn	
1800							1805						1810			1815
TTG	AAA	AAT	AAT	TCC	AAG	GAC	TTC	AAT	GAT	AAG	CTC	CCA	AAT	AAT	GAA	5526
Leu	Lys	Asn	Asn	Ser	Lys	Asp	Phe	Asn	Asp	Lys	Leu	Pro	Asn	Asn	Glu	
1820							1825						1830			
GAT	AGA	GTC	AGA	GGA	AGT	TTT	GCT	TTT	GAT	TCA	CCT	CAT	CAT	TAC	ACG	5574
Asp	Arg	Val	Arg	Gly	Ser	Phe	Ala	Phe	Asp	Ser	Pro	His	His	Tyr	Thr	
1835							1840						1845			
CCT	ATT	GAA	GGA	ACT	CCT	TAC	TGT	TTT	TCA	CGA	AAT	GAT	TCT	TTG	AGT	5622
Pro	Ile	Glu	Gly	Thr	Pro	Tyr	Cys	Phe	Ser	Arg	Asn	Asp	Ser	Leu	Ser	
1850							1855						1860			
TCT	CTA	GAT	TTT	GAT	GAT	GAT	GTT	GAC	CTT	TCC	AGG	GAA	AAG	GCT		5670
Ser	Leu	Asp	Phe	Asp	Asp	Asp	Val	Asp	Leu	Ser	Arg	Glu	Lys	Ala		
1865							1870						1875			
GAA	TTA	AGA	AAG	GCA	AAA	GAA	AAT	AAG	GAA	TCA	GAG	GCT	AAA	GTT	ACC	5718
Glu	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Lys	Glu	Ser	Glu	Ala	Lys	Val	Thr	
1880							1885						1890			1895

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AGC CAC ACA GAA CTA ACC TCC AAC CAA CAA TCA GCT AAT AAG ACA CAA	5766
Ser His Thr Glu Leu Thr Ser Asn Gln Gln Ser Ala Asn Lys Thr Gln	
1900 1905 1910	
GCT ATT GCA AAG CAG CCA ATA AAT CGA GGT CAG CCT AAA CCC ATA CTT	5814
Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly Gln Pro Lys Pro Ile Leu	
1915 1920 1925	
CAG AAA CAA TCC ACT TTT CCC CAG TCA TCC AAA GAC ATA CCA GAC AGA	5862
Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser Lys Asp Ile Pro Asp Arg	
1930 1935 1940	
GGG GCA GCA ACT GAT GAA AAG TTA CAG AAT TTT GCT ATT GAA AAT ACT	5910
Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn Phe Ala Ile Glu Asn Thr	
1945 1950 1955	
CCA GTT TGC TTT TCT CAT AAT TCC TCT CTG AGT TCT CTC AGT GAC ATT	5958
Pro Val Cys Phe Ser His Asn Ser Ser Leu Ser Ser Leu Ser Asp Ile	
1960 1965 1970 1975	
GAC CAA GAA AAC AAC AAT AAA GAA AAT GAA CCT ATC AAA GAG ACT GAG	6006
Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu Pro Ile Lys Glu Thr Glu	
1980 1985 1990	
CCC CCT GAC TCA CAG GGA GAA CCA AGT AAA CCT CAA GCA TCA GGC TAT	6054
Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys Pro Gln Ala Ser Gly Tyr	
1995 2000 2005	
GCT CCT AAA TCA TTT CAT GTT GAA GAT ACC CCA GTT TGT TTC TCA AGA	6102
Ala Pro Lys Ser Phe His Val Glu Asp Thr Pro Val Cys Phe Ser Arg	
2010 2015 2020	
AAC AGT TCT CTC AGT TCT CTT AGT ATT GAC TCT GAA GAT GAC CTG TTG	6150
Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp Ser Glu Asp Asp Leu Leu	
2025 2030 2035	
CAG GAA TGT ATA AGC TCC GCA ATG CCA AAA AAG AAA AAG CCT TCA AGA	6198
Gln Glu Cys Ile Ser Ser Ala Met Pro Lys Lys Lys Pro Ser Arg	
2040 2045 2050 2055	
CTC AAG GGT GAT AAT GAA AAA CAT AGT CCC AGA AAT ATG GGT GGC ATA	6246
Leu Lys Gly Asp Asn Glu Lys His Ser Pro Arg Asn Met Gly Gly Ile	
2060 2065 2070	
TTA GGT GAA GAT CTG ACA CTT GAT TTG AAA GAT ATA CAG AGA CCA GAT	6294
Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys Asp Ile Gln Arg Pro Asp	
2075 2080 2085	
TCA GAA CAT GGT CTA TCC CCT GAT TCA GAA AAT TTT GAT TGG AAA GCT	6342
Ser Glu His Gly Leu Ser Pro Asp Ser Gln Asn Phe Asp Trp Lys Ala	
2090 2095 2100	
ATT CAG GAA GGT GCA AAT TCC ATA GTA AGT AGT TTA CAT CAA GCT GCT	6390
Ile Gln Glu Gly Ala Asn Ser Ile Val Ser Ser Leu His Gln Ala Ala	
2105 2110 2115	
GCT GCT GCA TGT TTA TCT AGA CAA GCT TCG TCT GAT TCA GAT TCC ATC	6438
Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser Ser Asp Ser Asp Ser Ile	
2120 2125 2130 2135	
CTT TCC CTG AAA TCA GGA ATC TCT CTG GGA TCA CCA TTT CAT CTT ACA	6486
Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly Ser Pro Phe His Leu Thr	
2140 2145 2150	
CCT GAT CAA GAA GAA AAA CCC TTT ACA AGT AAT AAA GGC CCA CGA ATT	6534
Pro Asp Gln Glu Gln Lys Pro Phe Thr Ser Asn Lys Gly Pro Arg Ile	
2155 2160 2165	
CTA AAA CCA GGG GAG AAA AGT ACA TTG GAA ACT AAA AAG ATA GAA TCT	6582
Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu Thr Lys Lys Ile Glu Ser	
2170 2175 2180	
GAA AGT AAA GGA ATC AAA GGA GGA AAA AAA GTT TAT AAA AGT TTG ATT	6630
Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys Val Tyr Lys Ser Leu Ile	
2185 2190 2195	
ACT GGA AAA GTT CGA TCT AAT TCA GAA ATT TCA GGC CAA ATG AAA CAG	6678
Thr Gly Lys Val Arg Ser Asn Ser Glu Ile Ser Gln Gln Met Lys Gln	
2200 2205 2210 2215	

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CCC	CTT	CAA	GCA	AAC	ATG	CCT	TCA	ATC	TCT	CGA	GGC	AGG	ACA	ATG	ATT	6726
Pro	Leu	Gln	Ala	Asn	Met	Pro	Ser	Ile	Ser	Arg	Arg	Gly	Arg	Thr	Met	Ile
2220									2225						2230	
CAT	ATT	CCA	GGA	GTT	CGA	AAT	AGC	TCC	TCA	AGT	ACA	AGT	CCT	GTT	TCT	6774
His	Ile	Pro	Gly	Val	Arg	Asn	Ser	Ser	Ser	Ser	Thr	Ser	Pro	Val	Ser	
2235								2240						2245		
AAA	AAA	GGC	CCA	CCC	CTT	AAG	ACT	CCA	GCC	TCC	AAA	AGC	CCT	AGT	GAA	6822
Lys	Lys	Gly	Pro	Pro	Leu	Lys	Thr	Pro	Ala	Ser	Lys	Ser	Pro	Ser	Glu	
2250							2255						2260			
GGT	CAA	ACA	GCC	ACC	ACT	TCT	CCT	AGA	GGA	GCC	AAG	CCA	TCT	GTG	AAA	6870
Gly	Gln	Thr	Ala	Thr	Thr	Ser	Pro	Arg	Gly	Ala	Lys	Pro	Ser	Val	Lys	
2265							2270						2275			
TCA	GAA	TTA	AGC	CCT	GTT	GCC	AGG	CAG	ACA	TCC	CAA	ATA	GGT	GGG	TCA	6918
Ser	Glu	Leu	Ser	Pro	Val	Ala	Arg	Gln	Thr	Ser	Gln	Ile	Gly	Gly	Ser	
2280							2285				2290			2295		
AGT	AAA	GCA	CCT	TCT	AGA	TCA	GGA	TCT	AGA	GAT	TCG	ACC	CCT	TCA	AGA	6966
Ser	Lys	Ala	Pro	Ser	Arg	Ser	Gly	Ser	Arg	Asp	Ser	Thr	Pro	Ser	Arg	
2300							2305						2310			
CCT	GCC	CAG	CAA	CCA	TTA	AGT	AGA	CCT	ATA	CAG	TCT	CCT	GGC	CGA	AAC	7014
Pro	Ala	Gln	Gln	Pro	Leu	Ser	Arg	Pro	Ile	Gln	Ser	Pro	Gly	Arg	Asn	
2315							2320						2325			
TCA	ATT	TCC	CCT	GGT	AGA	AAT	GGA	ATA	AGT	CCT	CCT	AAC	AAA	TTA	TCT	7062
Ser	Ile	Ser	Pro	Gly	Arg	Asn	Gly	Ile	Ser	Pro	Pro	Asn	Lys	Leu	Ser	
2330							2335						2340			
CAA	CTT	CCA	AGG	ACA	TCA	TCC	CCT	AGT	ACT	GCT	TCA	ACT	AAG	TCC	TCA	7110
Gln	Leu	Pro	Arg	Thr	Ser	Ser	Pro	Ser	Thr	Ala	Ser	Thr	Lys	Ser	Ser	
2345							2350						2355			
GGT	TCT	GGA	AAA	ATG	TCA	TAT	ACA	TCT	CCA	GGT	AGA	CAG	ATG	AGC	CAA	7158
Gly	Ser	Gly	Lys	Met	Ser	Tyr	Thr	Ser	Pro	Gly	Arg	Gln	Met	Ser	Gln	
2360							2365						2370			
CAG	AAC	CTT	ACC	AAA	CAA	ACA	GGT	TTA	TCC	AAG	AAT	GCC	AGT	AGT	ATT	7206
Gln	Asn	Leu	Thr	Lys	Gln	Thr	Gly	Leu	Ser	Lys	Asn	Ala	Ser	Ser	Ile	
2380							2385						2390			
CCA	AGA	AGT	GAG	TCT	GCC	TCC	AAA	GGA	GTA	AAT	CAG	ATG	AAT	AAT	GGT	7254
Pro	Arg	Ser	Glu	Ser	Ala	Ser	Lys	Gly	Leu	Asn	Gln	Met	Asn	Asn	Gly	
2395							2400						2405			
AAT	GGA	GCC	AAT	AAA	AAG	GTA	GAA	CTT	TCT	AGA	ATG	TCT	TCA	ACT	AAA	7302
Asn	Gly	Ala	Asn	Lys	Lys	Val	Glu	Leu	Ser	Arg	Met	Ser	Ser	Thr	Lys	
2410							2415						2420			
TCA	AGT	GGA	AGT	GAA	TCT	GAT	AGA	TCA	GAA	AGA	CCT	GTA	TTA	GTA	CGC	7350
Ser	Ser	Gly	Ser	Glu	Ser	Asp	Arg	Ser	Gly	Arg	Ser	Val	Leu	Val	Arg	
2425							2430						2435			
CAG	TCA	ACT	TTC	ATC	AAA	GAA	GCT	CCA	AGC	CCA	ACC	TTA	AGA	AGA	AAA	7398
Gln	Ser	Thr	Phe	Ile	Lys	Glu	Ala	Pro	Ser	Pro	Thr	Leu	Arg	Arg	Lys	
2440							2445						2450			
TTG	GAG	GAA	TCT	GCT	TCA	TTT	GAA	TCT	TTT	TCT	CCA	TCA	TCT	AGA	CCA	7446
Leu	Glu	Glu	Ser	Ala	Ser	Phe	Glu	Ser	Leu	Ser	Pro	Ser	Ser	Arg	Pro	
2460							2465						2470			
GCT	TCT	CCC	ACT	AGG	TCC	CAG	GCA	CAA	ACT	CCA	GTT	TTA	AGT	CCT	TCC	7494
Ala	Ser	Pro	Thr	Arg	Ser	Gln	Ala	Gln	Thr	Pro	Val	Leu	Ser	Pro	Ser	
2475							2480						2485			
CTT	CCT	GAT	ATG	TCT	CTA	TCC	ACA	CAT	TCG	TCT	GTT	CAG	GCT	GGT	GGA	7542
Leu	Pro	Asp	Met	Ser	Leu	Ser	Tbr	His	Ser	Ser	Val	Gln	Ala	Gly	Gly	
2490							2495						2500			
TGG	CGA	AAA	CTC	CCA	CCT	AAT	CTC	AGT	CCC	ACT	ATA	GAG	TAT	AAT	GAT	7590
Tyr	Arg	Lys	Leu	Pro	Pro	Asn	Leu	Ser	Pro	Thr	Ile	Glu	Tyr	Asn	Asp	
2505							2510						2515			
GGA	AGA	CCA	GCA	AAG	CGC	CAT	GAT	ATT	GCA	CGG	TCT	CAT	TCT	GAA	AGT	7638
Gly	Arg	Pro	Ala	Lys	Arg	His	Asp	Ile	Ala	Arg	Ser	His	Ser	Glu	Ser	
2520							2525						2530			

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ATTACAAC TG CTATATAGAC	ATTTTGT T CAA	AAATGAAACT	TTAAAAGACT	GA AAAAATTT	8662	
GTAAATAGGT	TTGATTCTTG	TTAGAGGGTT	TTTGTCTGG	AAGCCATATT	TGATAGTATA	8722
CTTTGTCTTC	ACTGGTCTTA	TTTGGGAGG	CACTCTGAT	GGTAGGAAA	AAATAGAAAG	8782
CCAAGTATGT	TTGTACAGTA	TGTTTACAT	GTATTTAAAG	TAGCATCCC	TCCCAACTTC	8842
CTTAATTATT	GCTTGTCTAA	AATAATGAAC	ACTACAGATA	GGAAATATGA	TATATTGCTG	8902
TTATCAATCA	TTTCTAGATT	ATAAACTGAC	TAAACTTACA	TCAGGGAAA	ATTGGTATT	8962
ATGCAAAAAA	AAAATGTTT	TGTCCTGTG	AGTCCATCTA	ACATCATAAT	TAATCATGTG	9022
GCTGTGAAAT	TCACAGTAAT	ATGGTCCCCG	ATGAACAACT	TTACCCAGCC	TGCTTGCTT	9082
ACTGCATGAA	TGAAACTGAT	GGTTCAATT	CAGAAGTAAT	GATTAACAGT	TATGTGGTCA	9142
CATGATGTGC	ATAGAGATAG	CTACAGTGT	ATAATTACA	CTATTTGTG	CTCCAAACAA	9202
AACAAAATC	TGTGTAAC TG	TAACACATG	AATGAAACTA	TTTACCTGA	ACTAGATTT	9262
ATCTGAAAGT	AGGTAGAATT	TTTGCTATG	TGTAATTGT	TGTATATTCT	GGTATTGAG	9322
GTGAGATGGC	TGCTCTTTAT	TAATGAGACA	TGAATTGTG	CTCAACAGAA	ACTAAATGAA	9382
CATTTCA GAA	TAATTATTG	CTGTATGTA	ACTGTTACTG	AAATTGGTAT	TTGTTGAAG	9442
GGTTTGT T C	ACATTGTAT	TAATTAATTG	TTAAATG	CTCTTTAAA	AGCTTATATA	9502
AATTTTTCT	TCAGCTTCTA	TGCATTAAGA	GTAAAATTCC	TCTTACTGTA	ATAAAAACAT	9562
TGAAGAAGAC	TGTTGCCACT	TAACCATTCC	ATGCGTTGGC	ACTT		9606

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2843 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ala	Ala	Ser	Tyr	Asp	Gln	Leu	Leu	Lys	Gln	Val	Glu	Ala	Leu
1							5			10				15	
Lys	Met	Glu	Asn	Ser	Asn	Leu	Arg	Gln	Glu	Leu	Glu	Asp	Asn	Ser	Asn
	20						25						30		
His	Leu	Thr	Lys	Leu	Glu	Thr	Glu	Ala	Ser	Asn	Met	Lys	Glu	Val	Leu
	35						40					45			
Lys	Gln	Leu	Gln	Gly	Ser	Ile	Glu	Asp	Glu	Ala	Met	Ala	Ser	Ser	Gly
	50					55					60				
Gln	Ile	Asp	Leu	Leu	Glu	Arg	Leu	Lys	Glu	Leu	Asn	Leu	Asp	Ser	Ser
	65					70					75			80	
Asn	Phe	Pro	Gly	Val	Lys	Leu	Arg	Ser	Lys	Met	Ser	Leu	Arg	Ser	Tyr
	85					90						95			
Gly	Ser	Arg	Glu	Gly	Ser	Val	Ser	Ser	Arg	Ser	Gly	Glu	Cys	Ser	Pro
	100					105						110			
Val	Pro	Met	Gly	Ser	Phe	Pro	Arg	Arg	Gly	Phe	Val	Asn	Gly	Ser	Arg
	115					120						125			
Glu	Ser	Thr	Gly	Tyr	Leu	Glu	Glu	Leu	Glu	Lys	Glu	Arg	Ser	Leu	Leu
	130					135					140				
Leu	Ala	Asp	Leu	Asp	Lys	Glu	Glu	Lys	Glu	Lys	Asp	Trp	Tyr	Tyr	Ala
	145					150					155				160
Gln	Leu	Gln	Asn	Leu	Thr	Lys	Arg	Ile	Asp	Ser	Leu	Pro	Leu	Thr	Glu
	165					170						175			
Asn	Phe	Ser	Leu	Gln	Thr	Asp	Leu	Thr	Arg	Arg	Gln	Leu	Glu	Tyr	Glu

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180	185	190
Ala Arg Gln Ile Arg Val Ala Met	Glu Glu Gln Leu Gly	Thr Cys Gln
195 200	205	
Asp Met Glu Lys Arg Ala Gln Arg Arg	Ile Ala Arg Ile Gln Gln Ile	
210 215	220	
Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu	Leu Gln Ser Gln Ala Thr	
225 230	235	240
Glu Ala Glu Arg Ser Ser Gln Asn Lys His	Glu Thr Gly Ser His Asp	
245 250	255	
Ala Glu Arg Gln Asn Glu Gly Gln Gly	Val Gly Glu Ile Asn Met Ala	
260 265	270	
Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg	Arg Met Asp His Glu Thr	
275 280	285	
Ala Ser Val Leu Ser Ser Ser Ser Thr His	Ser Ala Pro Arg Arg Leu	
290 295	300	
Thr Ser His Leu Gly Thr Lys Val Glu Met	Val Tyr Ser Leu Leu Ser	
305 310	315	320
Met Leu Gly Thr His Asp Lys Asp Asp	Met Ser Arg Thr Leu Leu Ala	
325 330	335	
Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met	Arg Gln Ser Gly Cys	
340 345	350	
Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn	Asp Lys Asp Ser Val	
355 360	365	
Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala	Arg Ala Arg Ala Ser	
370 375	380	
Ala Ala Leu His Asn Ile Ile His Ser Gln Pro	Asp Asp Lys Arg Gly	
385 390	395	400
Arg Arg Glu Ile Arg Val Leu His Leu Leu Glu	Gln Ile Arg Ala Tyr	
405 410	415	
Cys Glu Thr Cys Trp Glu Trp Gln Gln Ala His	Glu Pro Gly Met Asp	
420 425	430	
Gln Asp Lys Asn Pro Met Pro Ala Pro Val Glu	His Gln Ile Cys Pro	
435 440	445	
Ala Val Cys Val Leu Met Lys Leu Ser Phe Asp	Glu Glu His Arg His	
450 455	460	
Ala Met Asn Glu Leu Gly Leu Gln Ala Ile	Ala Glu Leu Leu Gln	
465 470	475	480
Val Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp	His Tyr Ser Ile Thr	
485 490	495	
Leu Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn	Leu Thr Phe Gly Asp	
500 505	510	
Val Ala Asn Lys Ala Thr Leu Cys Ser Met Lys	Gly Cys Met Arg Ala	
515 520	525	
Leu Val Ala Gln Leu Lys Ser Glu Ser Glu Asp	Leu Gln Gln Val Ile	
530 535	540	
Ala Ser Val Leu Arg Asn Leu Ser Trp Arg Ala	Asp Val Asn Ser Lys	
545 550	555	560
Lys Thr Leu Arg Glu Val Gly Ser Val Lys Ala	Leu Met Glu Cys Ala	
565 570	575	
Leu Glu Val Lys Lys Glu Ser Thr Leu Lys Ser	Val Leu Ser Ala Leu	
580 585	590	
Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys	Ala Asp Ile Cys Ala	
595 600	605	

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Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser
 610 615 620
 Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg
 625 630 635 640
 Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu
 645 650 655
 Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His
 660 665 670
 Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser
 675 680 685
 Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val
 690 695 700
 Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met
 705 710 715 720
 Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys
 725 730 735
 Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu
 740 745 750
 His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His
 755 760 765
 Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser
 770 775 780
 His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val
 785 790 795 800
 Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr
 805 810 815
 Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro
 820 825 830
 Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys
 835 840 845
 Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His
 850 855 860
 Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile
 865 870 875 880
 Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala
 885 890 895
 Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu
 900 905 910
 His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala
 915 920 925
 His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn
 930 935 940
 Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser
 945 950 955 960
 Asn Asp Ser Leu Asn Ser Val Ser Ser Asn Asp Gly Tyr Gly Lys Arg
 965 970 975
 Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser
 980 985 990
 Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile
 995 1000 1005
 His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro
 1010 1015 1020
 Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg
 1025 1030 1035 1040

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Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile
 1045 1050 1055
 Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser
 1060 1065 1070
 Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys
 1075 1080 1085
 Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser
 1090 1095 1100
 Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly
 1105 1110 1115 1120
 Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu
 1125 1130 1135
 Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln
 1140 1145 1150
 His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu
 1155 1160 1165
 Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala
 1170 1175 1180
 Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser
 1185 1190 1195 1200
 Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Glu
 1205 1210 1215
 Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His
 1220 1225 1230
 Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr
 1235 1240 1245
 Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val
 1250 1255 1260
 Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu
 1265 1270 1275 1280
 Ser Ser Ala Glu Asp Gln Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala
 1285 1290 1295
 Asp Ser Ala Asn Thr Leu Gln Ile Ala Gln Ile Lys Gly Lys Ile Gly
 1300 1305 1310
 Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln
 1315 1320 1325
 His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser
 1330 1335 1340
 Glu Ser Ala Arg His Lys Ala Val Glu Phe Pro Ser Gly Ala Lys Ser
 1345 1350 1355 1360
 Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr
 1365 1370 1375
 Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser
 1380 1385 1390
 Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu
 1395 1400 1405
 Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro
 1410 1415 1420
 Asp Ser Pro Gly Gln Tbr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro
 1425 1430 1435 1440
 Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys
 1445 1450 1455
 Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val

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1460	1465	1470
Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu		
1475 1480 1485		
Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser		
1490 1495 1500		
Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val		
1505 1510 1515 1520		
Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu		
1525 1530 1535		
Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu		
1540 1545 1550		
Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp		
1555 1560 1565		
Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro		
1570 1575 1580		
Thr Lys Ser Ser Arg Lys Gly Lys Lys Pro Ala Gln Thr Ala Ser Lys		
1585 1590 1595 1600		
Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys		
1605 1610 1615		
Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe		
1620 1625 1630		
Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro		
1635 1640 1645		
Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser		
1650 1655 1660		
Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln		
1665 1670 1675 1680		
Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser		
1685 1690 1695		
Thr Asp Glu Ala Gln Gly Lys Thr Ser Ser Val Thr Ile Pro Glu		
1700 1705 1710		
Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile		
1715 1720 1725		
Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys		
1730 1735 1740		
Lys Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro		
1745 1750 1755 1760		
Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Pro Thr Ser Pro Val		
1765 1770 1775		
Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn		
1780 1785 1790		
Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn		
1795 1800 1805		
Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn		
1810 1815 1820		
Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe		
1825 1830 1835 1840		
Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe		
1845 1850 1855		
Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Asp Val		
1860 1865 1870		
Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys		
1875 1880 1885		

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Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln 1890 1895 1900	
Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg 1905 1910 1915 1920	
Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser 1925 1930 1935	
Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln 1940 1945 1950	
Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser 1955 1960 1965	
Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn 1970 1975 1980	
Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser 1985 1990 1995 2000	
Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp 2005 2010 2015	
Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile 2020 2025 2030	
Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro 2035 2040 2045	
Lys Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser 2050 2055 2060	
Pro Arg Asn Met Gly Gly Ile Leu Gln Asp Leu Thr Leu Asp Leu 2065 2070 2075 2080	
Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser 2085 2090 2095	
Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val 2100 2105 2110	
Ser Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala 2115 2120 2125	
Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu 2130 2135 2140	
Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr 2145 2150 2155 2160	
Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu 2165 2170 2175	
Glu Thr Lys Lys Ile Glu Ser Gln Ser Lys Gly Ile Lys Gly Gly Lys 2180 2185 2190	
Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu 2195 2200 2205	
Ile Ser Gln Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile 2210 2215 2220	
Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser 2225 2230 2235 2240	
Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro 2245 2250 2255	
Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg 2260 2265 2270	
Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln 2275 2280 2285	
Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser 2290 2295 2300	
Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro 2305 2310 2315 2320	

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Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile
 2325 2330 2335
 Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser
 2340 2345 2350
 Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser
 2355 2360 2365
 Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu
 2370 2375 2380
 Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly
 2385 2390 2395 2400
 Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu
 2405 2410 2415
 Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser
 2420 2425 2430
 Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro
 2435 2440 2445
 Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser
 2450 2455 2460
 Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln
 2465 2470 2475 2480
 Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His
 2485 2490 2495
 Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser
 2500 2505 2510
 Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile
 2515 2520 2525
 Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser
 2530 2535 2540
 Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg
 2545 2550 2555 2560
 Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala
 2565 2570 2575
 Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val
 2580 2585 2590
 Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala
 2595 2600 2605
 Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn
 2610 2615 2620
 Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser
 2625 2630 2635 2640
 Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp
 2645 2650 2655
 Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly
 2660 2665 2670
 Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu
 2675 2680 2685
 Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln
 2690 2695 2700
 Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn
 2705 2710 2715 2720
 Arg Leu Thr Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr
 2725 2730 2735
 Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn

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2740	2745	2750
Glu Ser Pro Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser		
2755	2760	2765
Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe		
2770	2775	2780
Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala		
2785	2790	2795
Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg		
2805	2810	2815
Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys		
2820	2825	2830
Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val		
2835	2840	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DP1(TB2)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCA GTC GCC GCT CCA GTC TAT CCG GCA CTA GGA ACA GCC CCG GGN GGC	48
Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly	
1 5 10 15	
GAG ACG GTC CCC GCC ATG TCT GCG GCC ATG AGG GAG AGG TTC GAC CGG	96
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg	
20 25 30	
TTC CTG CAC GAG AAG AAC TGC ATG ACT GAC CTT CTG GCC AAG CTC GAG	144
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu	
35 40 45	
GCC AAA ACC GGC GTG AAC AGG AGC TTC ATC GCT CTT GGT GTC ATC GGA	192
Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly	
50 55 60	
CTG GTG GCC TTG TAC CTG GTG TTC GGT TAT GGA GCC TCT CTC CTC TGC	240
Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys	
65 70 75 80	
AAC CTG ATA GGA TTT GGC TAC CCA GCC TAC ATC TCA ATT AAA GCT ATA	288
Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile	
85 90 95	
GAG AGT CCC AAC AAA GAA GAT GAT ACC CAG TGG CTG ACC TAC TGG GTA	336
Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu Thr Tyr Trp Val	
100 105 110	
GTG TAT GGT GTG TTC AGC ATT GCT GAA TTC TTC TCT GAT ATC TTC CTG	384
Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu	
115 120 125	
TCA TGG TTC CCC TTC TAC TAC ATG CTG AAG TGT GGC TTC CTG TTG TGG	432
Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp	
130 135 140	
TGC ATG GCC CCG AGC CCT TCT AAT GGG GCT GAA CTG CTC TAC AAG CGC	480

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Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg
 145 150 155 160
 ATC ATC CGT CCT TTC TTC CTG AAG CAC GAG TCC CAG ATG GAC AGT GTG 528
 Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val
 165 170 175
 GTC AAG GAC CTT AAA GAC AAG TCC AAA GAG ACT GCA GAT GCC ATC ACT 576
 Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr
 180 185 190
 AAA GAA GCG AAG AAA GCT ACC GTG AAT TTA CTG GGT GAA GAA AAG AAG 624
 Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys
 195 200 205
 AGC ACC TAAACCAAGAC TAAACCAAGAC TGGATGGAAA CTTCCGTGCC CTCCTGTACC 680
 Ser Thr
 210
 TTCCCTACTGG AGCTTGATGT TATATTAGGG ACTGTGGTAT AATTATTTA ATAATGTTGC 740
 CTTGGAAACA TTTTGAGAT ATTAAGATT GGAATGTGTT GTAAGTTCT TTGCTTACTT 800
 TTACTGTCTA TATATATAGG GAGCACTTTA AACTTAATGC AGTGGGCAGT GTCCACGTT 860
 TTGGAAAATG TATTTGCCT CTGGGTAGGA AAAGATGTAT GTTGCTATCC TGCAGGAAAT 920
 ATAAACCTAA AATAAAATTA TATACCCAC AGGCTGTGTA CTTTACTGGG CTCTCCCTGC 980
 ACGSATTTTC TCTGTAGTTA CATTAGGRT AATCTTATG GTTCTACTTC CTRTAATGTA 1040
 CAATTTATA TAATTGNGRA ATGTTTTAA TGTTTTGTG CACATGTACA TATGGAAATG 1100
 TTACTGTCTG ACTACANCAT GCATCATGCT CATGGGGAGG GAGCAGGGGA AGGTTGTATG 1160
 TGTCAATTAT AACTTCTGTA CAGTAAGACC ACCTGCCAAA AGCTGGAGGA ACCATTGTGC 1220
 TGGTGTGGTC TACTAAATAA TACTTAGGA AATACGTGAT TAATATGCAA GTGAACAAAG 1280
 TGAGAAATGA AATCGAATGG AGATTOGCCT GGTTGTTCC GTAGTATATG GCATATGAAT 1340
 ACCAGGATAG CTTATAAAAG CAGTTAGTTA GTTAGTTACT CACTCTAGTG ATAAATCGGG 1400
 AAATTTACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAG 1460
 AGTACCCCTGT AACTCTCAAT TCCCTGAAAA ACAGTAATA CTGTCTTATC TGCTATAAAC 1520
 TTTACATATT TGTCTATTGT CAAGATGCTA CANTGGAMNC CATTCTGGT TTTATCTCA 1580
 NAGGGAGAN ACATGTTGAT TTAGTCTTCT TTCCCAATCT TCTTTTTAA MCCAGTTNA 1640
 GGMMNCTCTG RAGATTTG Y C CACCTCTGAT TACATGTATG TTCT Y GTTG TATCATKAGC 1700
 AACAAACATGC TAATGRCGAC ACCTAGCTGT RAGMGCAATT CTGGGAGANT GARAGGNWGT 1760
 ATARAGTMNC CCATAATCTG CTTGGCAATA GTTAAGTCAA TCTATCTCA GTTTTTCTCT 1820
 GGCCTTAAAG GTCAACACACA AGAGGGCTCC GTAGTTTACA AGTCAGAGTC ACTTGTAGTC 1880
 CATTAAATG CCCTCATCCG TATTCTTGT GTTGATAAGC TGCACAKGAC TACATAGTAA 1940
 GTACAGANCA GTAAAGTTAA NNCGGATGTC TCCATTGATC TGCCAANTCG NTATAGAGAG 2000
 CAATTGTCT GGACTAGAGAA ATCTGAGTT TACACCATAAC TGTTAAGAGT CCTTTGAAAT 2060
 TAAACTAGAC TAAAACAAGT GTATAACTAA ACTAACAAAGA TTAAATATCC AGCCAGTACA 2120
 GTATTTTTA AGGCAAATAA AGATGATTAG CTCACCTTGA GNTAACAAATC AGGTAAGATC 2180
 ATNACAATGT CTCATGATGT NAANAATATT AAAGATATCA ATACTAAGTG ACAGTATCAC 2240
 NNCTAAATATA ATATGGATCA GAGCATTAT TTTGGGGAGG AAAACAGTGG TGATTACCGG 2300
 CATTAAATTA AACTTAAAC TTTGTAGAAA GCAACAAAAA TTGTTCTTGG GAGAAAATCA 2360
 ACTTTAGAT TAAAAAAATT TTAAGTAWCT AGGAGTATT AAATCCTTTT CCCATAAATA 2420
 AAAGTACAGT TTTCTTGGTG GCAGAATGAA AATCAGCAAC NTCTACCATAGACTATAT 2480
 AATCAGATTG ACAGCATATA GAATATATTA TCAGACAAGA TGAGGAGGTA CAAAAGTTAC 2540

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TATTGCTCAT AATGACTTAC AGGCTAAAAN TAGNTNTAAA ATACTATATT AAATTCTGAA	2600
TGCAATTTT TTTTGTTCGC TTGAGACCAA AATTAAAGTT AACTGTTGCT GGCAGTCTAA	2660
GTGTAAATGT TAACAGCAGG AGAAGTTAAG AATTGAGCAG TTCTGTTGCA TGATTTCCCA	2720
AATGAAATAC TGCCTGGCT AGAGTTGAA AAACATAATTG AGCCTGTGCC TGGCTAGAAA	2780
ACAAGCGTT ATTTGAATGT GAATAGTGT TCAAAGGTAT GTAGTTACAG AATTCCCTACC	2840
AAACAGCTTA AATTCTTCAA AAAGAATTG CTGCAGCAGT TATTCCCTTA CCTGAAGGCT	2900
TCAATCATT GGATCAACAA CTGCTACTCT CGGGAAAGACT CCTCTACTCA CAGCTGAAGA	2960
AAATGAGCAC ACCCTTCACA CTGTTATCAC CTATCCTGAA GATGTGATAC ACTGAATGGA	3020
AATAAATAGA TGTAATAAAA ATTGAGWTCT CATTAAAAAA AAACCATGTG CCCAATGGGA	3080
AAATGACCTC ATGTTGTGGT TTAAACAGCA ACTGCACCCCA CTAGCACAGC CCATTGAGCT	3140
ANCCTATATA TACATCTCTG TCAGTGCCCC TC	3172

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly	15
1 5 10 15	
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Arg Phe Asp Arg	30
20 25 30	
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu	45
35 40 45	
Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly	60
50 55 60	
Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys	80
65 70 75 80	
Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile	95
85 90 95	
Glu Ser Pro Asn Lys Glu Asp Asp Thr Glu Trp Leu Thr Tyr Trp Val	110
100 105 110	
Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu	125
115 120 125	
Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp	140
130 135 140	
Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg	160
145 150 155 160	
Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Glu Met Asp Ser Val	175
165 170 175	
Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr	190
180 185 190	
Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys	205
195 200 205	
Ser Thr	
210	

(2) INFORMATION FOR SEQ ID NO:5:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TB1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val	Ala	Pro	Val	Val	Val	Gly	Ser	Gly	Arg	Ala	Pro	Arg	His	Pro	Ala	
1				5					10					15		
Pro	Ala	Ala	Met	His		Pro	Arg	Arg	Pro	Asp	Gly	Phe	Asp	Gly	Leu	Gly
			20					25						30		
Tyr	Arg	Gly	Gly	Ala	Arg	Asp	Glu	Gln	Gly	Phe	Gly	Gly	Ala	Phe	Pro	
	35					40						45				
Ala	Arg	Ser	Phe	Ser	Thr	Gly	Ser	Asp	Leu	Gly	His	Trp	Val	Thr	Thr	
	50				55					60						
Pro	Pro	Asp	Ile	Pro	Gly	Ser	Arg	Asn	Leu	His	Trp	Gly	Glu	Lys	Ser	
	65				70				75				80			
Pro	Pro	Tyr	Gly	Val	Pro	Thr	Thr	Ser	Thr	Pro	Tyr	Glu	Gly	Pro	Thr	
		85				90						95				
Glu	Glu	Pro	Phe	Ser	Ser	Gly	Gly	Gly	Ser	Val	Gln	Gly	Gln	Ser		
	100					105					110					
Ser	Glu	Gln	Leu	Asn	Arg	Phe	Ala	Gly	Phe	Ile	Gly	Leu	Ala	Ser		
	115					120					125					
Leu	Phe	Thr	Glu	Asn	Val	Leu	Ala	His	Pro	Cys	Ile	Val	Leu	Arg	Arg	
	130				135						140					
Gln	Cys	Gln	Val	Asn	Tyr	His	Ala	Gln	His	Tyr	His	Leu	Thr	Pro	Phe	
	145				150					155			160			
Thr	Val	Ile	Asn	Ile	Met	Tyr	Ser	Phe	Asn	Lys	Thr	Gln	Gly	Pro	Arg	
	165						170					175				
Ala	Leu	Trp	Lys	Gly	Met	Gly	Ser	Thr	Phe	Ile	Val	Gln	Gly	Val	Thr	
	180					185					190					
Leu	Gly	Ala	Glu	Gly	Ile	Ile	Ser	Gly	Phe	Thr	Pro	Leu	Pro	Arg	Glu	
	195					200					205					
Val	Leu	His	Lys	Trp	Ser	Pro	Lys	Gln	Ile	Gly	Glu	His	Leu	Leu	Leu	
	210				215					220						
Lys	Ser	Leu	Thr	Tyr	Val	Val	Ala	Met	Pro	Phe	Tyr	Ser	Ala	Ser	Leu	
	225				230					235				240		
Ile	Glu	Thr	Val	Gln	Ser	Glu	Ile	Ile	Arg	Asp	Asn	Thr	Gly	Ile	Leu	
	245					250						255				
Glu	Cys	Val	Lys	Glu	Gly	Ile	Gly	Arg	Val	Ile	Gly	Met	Gly	Val	Pro	
	260					265					270					
His	Ser	Lys	Arg	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Ile	Phe	Pro	Thr	Val	
	275					280					285					
Leu	His	Gly	Val	Leu	His	Tyr	Ile	Ile	Ser	Ser	Val	Ile	Gln	Lys	Phe	
	290				295						300					
Val	Leu	Leu	Ile	Leu	Lys	Arg	Lys	Thr	Tyr	Asn	Ser	His	Leu	Ala	Glu	
	305				310					315				320		
Ser	Thr	Ser	Pro	Val	Gln	Ser	Met	Leu	Asp	Ala	Tyr	Phe	Pro	Glu	Leu	
	325						330						335			
Ile	Ala	Asn	Phe	Ala	Ala	Ser	Leu	Cys	Ser	Asp	Val	Ile	Leu	Tyr	Pro	

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340	345	350	
Leu Glu Thr Val Leu His Arg	Leu His Ile Gln Gly	Thr Arg Thr Ile	
355	360	365	
Ile Asp Asn Thr Asp Leu Gly	Tyr Glu Val Leu Pro	Ile Asn Thr Gln	
370	375	380	
Tyr Glu Gly Met Arg Asp Cys	Ile Asn Thr Ile Arg Gln	Glu Gly	
385	390	395	400
Val Phe Gly Phe Tyr Lys Gly	Phe Gly Ala Val Ile Ile Gln	Tyr Thr	
405	410	415	
Leu His Ala Ala Val Leu Gln Ile Thr Lys Ile Ile Tyr Ser Thr Leu			
420	425	430	
Leu Gln			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: YS-39(TB2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Leu Arg Arg Phe Asp Arg Phe Leu His Glu Lys Asn Cys Met Thr	
1 5 10 15	
Asp Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn Arg Ser Phe	
20 25 30	
Ile Ala Leu Gly Val Ile Gly Leu Val Ala Leu Tyr Leu Val Phe Gly	
35 40 45	
Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Gly Tyr Pro Ala	
50 55 60	
Tyr Ile Ser Ile Lys Ala Ile Glu Ser Pro Asn Lys Glu Asp Asp Thr	
65 70 75 80	
Gln Trp Leu Thr Tyr Trp Val Val Tyr Gly Val Phe Ser Ile Ala Glu	
85 90 95	
Phe Phe Ser Asp Ile Phe Leu Ser Trp Phe Pro Phe Tyr Tyr Ile Leu	
100 105 110	
Lys Cys Gly Phe Leu Leu Trp Cys Met Ala Pro Ser Pro Ser Asn Gly	
115 120 125	
Ala Glu Leu Leu Tyr Lys Arg Ile Ile Arg Pro Phe Phe Leu Lys His	
130 135 140	
Glu Ser Gln Met Asp Ser Val Val Lys Asp Leu Lys Asp Lys Ala Lys	
145 150 155 160	
Glu Thr Ala Asp Ala Ile Thr Lys Glu Ala Lys Lys Ala Thr Val Asn	
165 170 175	
Leu Leu Gly Glu Glu Lys Lys Ser Thr	
180 185	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2842 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: protein

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(v i i) IMMEDIATE SOURCE:

(B) CLONE: APC

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu
 1 5 10 15

Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn
 20 25 30

His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu
 35 40 45

Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
 50 55 60

Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser
 65 70 75 80

Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr
 85 90 95

Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro
 100 105 110

Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg
 115 120 125

Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu
 130 135 140

Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala
 145 150 155 160

PRD

Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Leu Thr Glu Asn
 165 170 175

Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu Ala
 180 185 190

Arg Gln Ile Arg Val Ala Met Gln Gln Leu Gly Thr Cys Gln Asp
 195 200 205

Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu
 210 215 220

Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu
 225 230 235 240

Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp Ala
 245 250 255

Glu Arg Gln Asn Glu Gly Gln Gln Val Gly Glu Ile Asn Met Ala Thr
 260 265 270

Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr Ala
 275 280 285

Ser Val Leu Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu Thr
 290 295 300

Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser Met
 305 310 315 320

Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala Met
 325 330 335

Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys Leu
 340 345 350

Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val Leu

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355	360	365
Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser Ala		
370	375	380
Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly Arg		
385	390	400
Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr Cys		
405	410	415
Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp Gln		
420	425	430
Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro Ala		
435	440	445
Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His Ala		
450	455	460
Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln Val		
465	470	480
Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr Leu		
485	490	495
Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp Val		
500	505	510
Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala Leu		
515	520	525
Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile Ala		
530	535	540
Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys Lys		
545	550	560
Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala Leu		
565	570	575
Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu Trp		
580	585	590
Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala Val		
595	600	605
Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln		
610	615	620
Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Ile Leu Arg Asn		
625	630	640
Val Ser Ser Leu Ile Ala Thr Asn Gln Asp His Arg Gln Ile Leu Arg		
645	650	655
Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His Ser		
660	665	670
Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala		
675	680	685
Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val Ser		
690	695	700
Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met Gly		
705	710	720
Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr		
725	730	735
Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu His		
740	745	750
Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His Leu		
755	760	765
Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser His		
770	775	780

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Arg	Ser	Lys	Gln	Arg	His	Lys	Gln	Ser	Leu	Tyr	Gly	Asp	Tyr	Val	Phe
785					790				795						800
Asp	Thr	Asn	Arg	His	Asp	Asp	Asn	Arg	Ser	Asp	Asn	Phe	Asn	Thr	Gly
					805				810						815
Asn	Met	Thr	Val	Leu	Ser	Pro	Tyr	Leu	Asn	Thr	Thr	Val	Leu	Pro	Ser
								825							830
Ser	Ser	Ser	Ser	Arg	Gly	Ser	Leu	Asp	Ser	Ser	Arg	Ser	Glu	Lys	Asp
							840				845				
Arg	Ser	Leu	Glu	Arg	Glu	Arg	Gly	Ile	Gly	Leu	Gly	Asn	Tyr	His	Pro
					855					860					
Ala	Thr	Glu	Asn	Pro	Gly	Thr	Ser	Ser	Lys	Arg	Gly	Leu	Gln	Ile	Ser
						870				875					880
Thr	Thr	Ala	Ala	Gln	Ile	Ala	Lys	Val	Met	Glu	Glu	Val	Ser	Ala	Ile
					885				890						895
His	Thr	Ser	Gln	Glu	Asp	Arg	Ser	Ser	Gly	Ser	Thr	Thr	Glu	Leu	His
							905				910				
Cys	Val	Thr	Asp	Glu	Arg	Asn	Ala	Leu	Arg	Arg	Ser	Ser	Ala	Ala	His
						920				925					
Thr	His	Ser	Asn	Thr	Tyr	Asn	Phe	Thr	Lys	Ser	Glu	Asn	Ser	Asn	Arg
						935				940					
Thr	Cys	Ser	Met	Pro	Tyr	Ala	Lys	Leu	Glu	Tyr	Lys	Arg	Ser	Ser	Asn
					950				955						960
Asp	Ser	Leu	Asn	Ser	Val	Ser	Ser	Ser	Asp	Gly	Tyr	Gly	Lys	Arg	Gly
					965				970						975
Gln	Met	Lys	Pro	Ser	Ile	Glu	Ser	Tyr	Ser	Glu	Asp	Asp	Glu	Ser	Lys
					980				985						990
Phe	Cys	Ser	Tyr	Gly	Gln	Tyr	Pro	Ala	Asp	Leu	Ala	His	Lys	Ile	His
						995		1000				1005			
Ser	Ala	Asn	His	Met	Asp	Asp	Asn	Asp	Gly	Glu	Leu	Asp	Thr	Pro	Ile
						1010		1015				1020			
Asn	Tyr	Ser	Leu	Lys	Tyr	Ser	Asp	Glu	Gln	Leu	Asn	Ser	Gly	Arg	Gln
					1025		1030			1035					1040
Ser	Pro	Ser	Gln	Asn	Glu	Arg	Trp	Ala	Arg	Pro	Lys	His	Ile	Ile	Glu
					1045				1050						1055
Asp	Glu	Ile	Lys	Gln	Ser	Glu	Glx	Arg	Gln	Ser	Arg	Asn	Gln	Ser	Thr
						1060		1065							1070
Thr	Tyr	Pro	Val	Tyr	Thr	Glu	Ser	Thr	Asp	Asp	Lys	His	Leu	Lys	Phe
						1075		1080				1085			
Gln	Pro	His	Phe	Gly	Gln	Gln	Glu	Cys	Val	Ser	Pro	Tyr	Arg	Ser	Arg
						1090		1095				1100			
Gly	Ala	Asn	Gly	Ser	Glu	Thr	Asn	Arg	Val	Gly	Ser	Asn	His	Gly	Ile
					1105		1110			1115					1120
Asn	Gln	Asn	Val	Ser	Gln	Ser	Ile	Cys	Gln	Glu	Asp	Asp	Tyr	Glu	Asp
					1125				1130						1135
Asp	Lys	Pro	Thr	Asn	Tyr	Ser	Glu	Arg	Tyr	Ser	Glu	Glu	Gln	His	
					1140		1145			1150					
Glu	Glu	Glu	Glu	Arg	Pro	Thr	Asn	Tyr	Ser	Ile	Lys	Tyr	Asn	Glu	Glu
					1155		1160			1165					
Lys	Arg	His	Val	Asp	Gln	Pro	Ile	Asp	Tyr	Ser	Leu	Lys	Tyr	Ala	Thr
					1170		1175			1180					
Asp	Ile	Pro	Ser	Ser	Gln	Lys	Gln	Ser	Phe	Ser	Phe	Ser	Lys	Ser	Ser
					1185		1190			1195					1200
Ser	Gly	Gln	Ser	Ser	Lys	Thr	Glu	His	Met	Ser	Ser	Ser	Ser	Glu	Asn
					1205				1210						1215

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Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His Pro
 1220 1225 1230
 Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys
 1235 1240 1245
 Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu
 1250 1255 1260
 Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser
 1265 1270 1275 1280
 Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp
 1285 1290 1295
 Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly Thr
 1300 1305 1310
 Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln His
 1315 1320 1325
 Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu
 1330 1335 1340
 Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser Pro
 1345 1350 1355 1360
 Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Val
 1365 1370 1375
 Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser Leu
 1380 1385 1390
 Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu Pro
 1395 1400 1405
 Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp
 1410 1415 1420
 Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Ser Lys Thr Pro Pro Pro
 1425 1430 1435 1440
 Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys Ala
 1445 1450 1455
 Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val Asn
 1460 1465 1470
 Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu Leu
 1475 1480 1485
 His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser
 1490 1495 1500
 Leu Ser Ala Leu Ser Leu Asp Gln Pro Phe Ile Gln Lys Asp Val Glu
 1505 1510 1515 1520
 Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu Thr
 1525 1530 1535
 Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala
 1540 1545 1550
 Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp
 1555 1560 1565
 Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro Thr
 1570 1575 1580
 Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu
 1585 1590 1595 1600
 Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu
 1605 1610 1615
 Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe Thr
 1620 1625 1630
 Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro Ile

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1635	1640	1645
Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro		
1650	1655	1660
Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln Ser		
1665	1670	1675
Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr		
1685	1690	1695
Asp Glu Ala Gln Gly Lys Thr Ser Ser Val Thr Ile Pro Glu Leu		
1700	1705	1710
Asp Asp Asn Lys Ala Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn		
1715	1720	1725
Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys Lys		
1730	1735	1740
Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro Asn		
1745	1750	1755
Lys Asn Gln Leu Asp Gly Lys Lys Lys Pro Thr Ser Pro Val Lys		
1765	1770	1775
Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala		
1780	1785	1790
Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn Lys		
1795	1800	1805
Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp		
1810	1815	1820
Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe Asp		
1825	1830	1840
Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser		
1845	1850	1855
Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val Asp		
1860	1865	1870
Leu Ser Arg Gln Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu		
1875	1880	1885
Ser Gln Ala Lys Val Thr Ser His Thr Gln Leu Thr Ser Asn Gln Gln		
1890	1895	1900
Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly		
1905	1910	1920
Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser		
1925	1930	1935
Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn		
1940	1945	1950
Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser Leu		
1955	1960	1965
Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu		
1970	1975	1980
Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys		
1985	1990	1995
Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp Thr		
2005	2010	2015
Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp		
2020	2025	2030
Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro Lys		
2035	2040	2045
Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser Pro		
2050	2055	2060

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Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys
 2065 2070 2075 2080
 Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser Glu
 2085 2090 2095
 Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val Ser
 2100 2105 2110
 Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser
 2115 2120 2125
 Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly
 2130 2135 2140
 Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr Ser
 2145 2150 2155 2160
 Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu
 2165 2170 2175
 Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Lys Lys
 2180 2185 2190
 Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu Ile
 2195 2200 2205
 Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile Ser
 2210 2215 2220
 Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser Ser
 2225 2230 2235 2240
 Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala
 2245 2250 2255
 Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly
 2260 2265 2270
 Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln Thr
 2275 2280 2285
 Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg
 2290 2295 2300
 Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile
 2305 2310 2315 2320
 Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gln Ile Ser
 2325 2330 2335
 Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr
 2340 2345 2350
 Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro
 2355 2360 2365
 Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser
 2370 2375 2380
 Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu
 2385 2390 2395 2400
 Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu Ser
 2405 2410 2415
 Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu
 2420 2425 2430
 Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser
 2435 2440 2445
 Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu
 2450 2455 2460
 Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr
 2465 2470 2475 2480
 Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His Ser
 2485 2490 2495

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Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro
 2500 2505 2510
 Thr Ile Gln Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile Ala
 2515 2520 2525
 Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly
 2530 2535 2540
 Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg Val
 2545 2550 2555 2560
 Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ile Leu Ser Ala Ser
 2565 2570 2575
 Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val Asn
 2580 2585 2590
 Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala Lys
 2595 2600 2605
 Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser
 2610 2615 2620
 Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys
 2625 2630 2635 2640
 Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp Val
 2645 2650 2655
 Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg
 2660 2665 2670
 Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu Lys
 2675 2680 2685
 Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn
 2690 2695 2700
 Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn Arg
 2705 2710 2715 2720
 Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr Glu
 2725 2730 2735
 Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn Glu
 2740 2745 2750
 Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Lys
 2755 2760 2765
 His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe Asn
 2770 2775 2780
 Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg
 2785 2790 2795 2800
 Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg Asp
 2805 2810 2815
 Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg
 2820 2825 2830
 His Ser Gln Ser Tyr Leu Val Thr Ser Val
 2835 2840

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(viii) IMMEDIATE SOURCE:

- (B) CLONE: ral2(yeast)

-continued

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu	Thr	Gly	Ala	Lys	Gly	Leu	Gln	Leu	Arg	Ala	Leu	Arg	Arg	Ile	Ala
1				5					10					15	
Arg	Ile	Glu	Gln	Gly	Gly	Thr	Ala	Ile	Ser	Pro	Thr	Ser	Pro	Leu	
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: m3(mAChR)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu	Tyr	Trp	Arg	Ile	Tyr	Lys	Glu	Thr	Glu	Lys	Arg	Thr	Lys	Glu	Leu
1				5					10					15	
Ala	Gly	Leu	Gln	Ala	Ser	Gly	Thr	Glu	Ala	Glu	Thr	Glu			
		20						25							

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: MCC

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu	Tyr	Pro	Asn	Leu	Ala	Glu	Glu	Arg	Ser	Arg	Trp	Glu	Lys	Glu	Leu
1				5					10					15	
Ala	Gly	Leu	Arg	Glu	Glu	Ala	Glu	Ser	Leu	Thr	Ala	Met			
		20						25							

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATCAAGAC TGTGACTTTT AATTGTAGTT TATCCATTT

(2) INFORMATION FOR SEQ ID NO:12:

-continued

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTT A G A A T T T C A T G T T A A T A T A T T G T G T T C T T T T T A A C A G

4 0

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:13:

G T A G A T T T T A A A A G G T G T T T A A A A T A A T A T T T T A A G C T

4 0

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:14:

A A G C A A T T G T T G T A T A A A A A C T T G T T T C T A T T T T A T T T A G

4 0

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:15:

G T A A C T T T T C T T C A T A T A G T A A A C A T T G C C T T G T G T A C T C

4 0

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

-continued

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:16:

NNNNNNNNNN NNNGTCCCTT TTTTTAAAAA AAAAAAAATAG

4 0

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAAGTAACT TGGCAGTACA ACTTATTTGA AACTTTAATA

4 0

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATACAAGATA TTGATACTTT TTTTATTATT GTGGTTTTAG

4 0

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAAGTTACT TGTTTCTAAG TGATAAAACA G Y GAAGAGCT

4 0

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATAAAAACA TAACTAATT A GGTTTCTTGT TTTATTTAG

4 0

-continued

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTTAGTAAAT TSCCTTTTT GTTTGTGGGT ATAAAAAATAG

4 0

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCATTTTG CATGTAATG TGTTAACCTCC ATCTTAACAG

4 0

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTAAATAAAAT TATTTTATCA TATTTTTTAA AAATTAATTA

4 0

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CATGATGTTA TCTGTATTTA CCTATAGTCT AAATTATACC ATCTATAATG TGCTTAATTT

6 0

TTAG

6 4

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTAACAGAAG ATTACAAACC CTGGTCAC TAATGCCATGAC TACTTTGCTA AG

5 2

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGATATTAAA GTCGTAATTT TGTTTCTAAA CTCATTTGGC CCACAG

4 6

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTATGTTCTC TATAGTGTAC ATCGTAGTGC ATGTTTCAAA

4 0

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATCATTGCT CTTCAAATAA CAAAGCATTA TGGTTATGT TGATTTTATT TTTCAG

5 6

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:29:

-continued

GTAAGACAAA AATGTTTTT AATGACATAG ACAATTACTG GTG

4 3

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTAGATGATT GTCTTTTCC TCTTGCCCTT TTTAAATTAG

4 0

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATGTTTT ATAACATGTA TTCTTAAGA TAGCTCAGGT ATGA

4 4

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTTGGCTTC AAGTTGNCTT TTTAAAGATTC CTCTATTCTG TATTTAATT ACAG

5 4

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTACTATTAA GAATTCACC TGTTTTCTT TTCTCTCTT TTCTTTGAGG CAGGGTCTCA

6 0

CTCTG

6 5

(2) INFORMATION FOR SEQ ID NO:34:

-continued

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAACTAGTA TGATTTATG TATAAATTAA TCTAAAATTG ATTAATTCC AG

5 2

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTACCTTTGA AAACATTTAG TACTATAATA TGAATTCAT GT

4 2

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCAACTCNAATTAGATGACC CATATTCAAGAACCTTACTAG

4 0

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATATAG AGTTTATAT TACTTTAAA GTACAGAATT CATACTCTCA AAAA

5 4

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

-continued

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATTGTGACCT TAATTTGTG ATCTCTTGAT TTTTATTCAG

4 1

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCCCCGGCTG CCGCTCTC

1 8

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCAGCGGGCGG CTCCCGTG

1 8

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGAACGGCT CTCATGCTGC

2 0

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGTGCGGGG AGGAATGGA

1 9

-continued

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGATATCTT ACCAAATGAT ATAC

2 4

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTATTCCTAC TTCTTCTATA CAG

2 3

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TACCCATGCT GGCTCTTTT C

2 1

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGGGCCATC TTGTTCTCTGA

2 0

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

-continued

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACATTA~~GG~~CA CAAAGCTTGC AA

2 2

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCAAGCTCC AGTAAGAAGG TA

2 2

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGC~~GG~~GCTCCT GGGTTGTTG

1 9

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCCC~~TT~~CCT TTCTGAGGAC

2 0

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTTCTCCTG CCTCTTACTG C

2 1

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(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGACACCCC CCATTCCTC

2 0

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCACTTAAAG CACATATATT TAGT

2 4

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTATGGAAAA TAGTGAAGAA CC

2 2

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCTTAAGTC CTGTTTTCT TTTG

2 4

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTT AGAACCT TTTT TGTGTT GTG

2 3

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTCAGATTAT ACAC TAAAGCC TAAC

2 4

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CATGTCTCTT ACAGTAGTAC CA

2 2

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGGTCCAAGG GTAGCCAAGG

2 0

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:60:

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TAAAAAATGGA TAAACTACAA TTAAAAG

2 7

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAATACAGAA TCATGTCTTG AAGT

2 4

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ACACCTAAAG ATGACAATT GAG

2 3

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAACTTAGAT AGCAGTAAATT TCCC

2 4

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACAATAAACT GGAGTACACA AGG

2 3

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs

-continued

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:65:

A T A G G T C A T T G C T T C T T G C T G A T

2 3

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:66:

T G A A T T T T A A T G G A T T A C C T A G G T

2 4

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:67:

C T T T T T T G C T T T A C T G A T T A A C G

2 5

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:68:

T G T A A T T C A T T T T A T T C C T A A T A G C T C

2 7

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

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(x i) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTAGCCATA GTATGATTAT TTCT

2 4

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTACCTATTT TTATAACCCAC AAAC

2 4

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGAAAGCCT ACACCATTTT TGC

2 3

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCATTCTT AGAACCATCT TGC

2 3

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACCTATAGTC TAAATTATAC CATC

2 4

(2) INFORMATION FOR SEQ ID NO:74:

119

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:74:

G T C A T G G C A T T A G T G A C C A G

2 0

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:75:

A G T C G T A A T T T T G T T T C T A A A C T C

2 4

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:76:

T G A A G G A C T C G G A T T T C A C G C

2 1

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:77:

T C A T T C A C T C A C A G C C T G A T G A C

2 3

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

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(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:78:

G C T T T G A A A C A T G C A C T A C G A T

2 2

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:79:

A A A C A T C A T T G C T C T T C A A A T T A A C

2 4

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:80:

T A C C A T G A T T T A A A A T C C A C C A G

2 4

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:81:

G A T G A T T G T C T T T T C C T C T T G C

2 3

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:82:

C T G A G C T A T C T T A A G A A A T A C A T G

2 4

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(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTTTAAATGA TCCTCTATTC TGTAT

2 5

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACAGAGTCAG ACCCTGCCTC AAAG

2 4

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTCTATTCT TACTGCTAGC ATT

2 3

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATACACAGGT AAGAAATTAG GA

2 2

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TAGATGACCC ATATTCTGTT TC

2 2

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAATTAGGTC TTTTGAGAG TA

2 2

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GT TACTGCAT ACACATTGTG AC

2 2

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTTTTTGTT TCCTAACATG AAG

2 3

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCCCCACAG GTAATACTCC C

2 1

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(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:92:

G C T A G A A C T G A A T G G G G T A C G

2 1

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:93:

C A G G A C A A A A T A A T C C T G T C C C

2 2

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:94:

A T T T T C T T A G T T T C A T T C T T C C T C

2 4

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:95:

A G A A G G A T C C C T T G T G C A G T G T G G A

2 5

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GACAGGATCC TGAAGCTGAG TTTG

2 4

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCAGAAAGTG CTGAAGAG

1 8

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGAATAATTA GGTCTCCAA

1 9

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCAAATCCTA AGAGAGAACAA

2 1

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:100:

131

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GATGGCAAGC TTGAGCCAG

19

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTTCCAGCAG TGTACACAG

18

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(v i) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGGAGATTTC GCTCCTGAA

18